

CONSENSUS
GRBP2
gi 7503594
gi 6093970
gi 543444
gi 6319363
gi 6225859
gi 1085218
gi 1175418

1 LLLERLRKKLEVELEKIREGAEKLLRLITSNEKV
38 ngraaLNQQLKAVRMRIKAENLLKVATNSKV
159 SKLVILQLELEKELKVKRGLEQFLRGAPDKS
42 SHRARLHQQISKELRMRTGAENLYRATSNW
216 LRIEELRHFRVEHVAEAGAKNVLRLLSAaKa
5 QLEQNIKKIAVEENIRGASALKKTSNMV
47 DIKDRIRKREIRKELKIKEGAENLRKVTTDKK
42 VERDRLRKEISRELKIKEGAELRRATTERK
38 KLEEDLKGKLEVECKIRDGAETLLQVFDTNFkktkerKEMLKKKCTDElessKKKIEEL

10 20 30 40 50 60

52
87
209
91
270
54
96
91
97

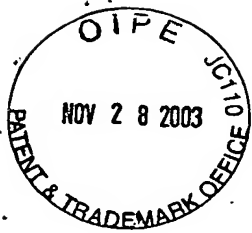
70

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53 KQSLERLKEHLH
88 KEELEGLNLSV
210 RMOIERLSQEA
92 KEELA-ELSTSV
271 RESLERLGLP
55 EDSLK-KLRKT
97 HHKLQ-ELNAHI
92 KQELD-GLETPP
98 VSSIE-SFQGEN

63
98
220
102
282
65
107
102
108

FIG. 1B



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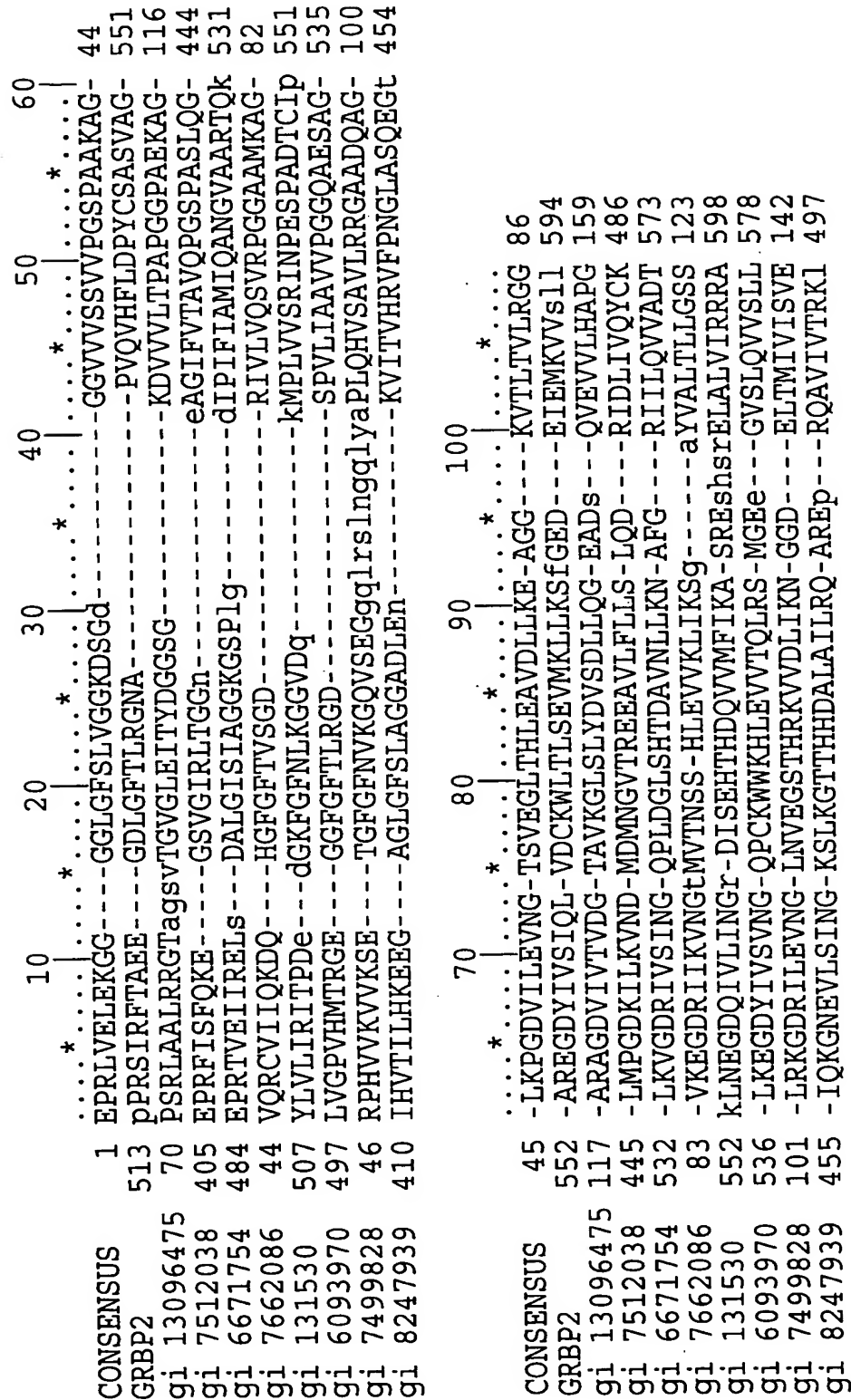
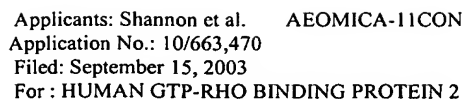


FIG. 1C



(AC008521)

EXONS

mRNA

AX077672

FIG. 2



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nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

tc	cgc	gcc	cgc	gcc	gct	agc	M	T	D	A	L	L	6
							ATG	ACC	GAC	GCG	CTG	TTG	38
P	A	A	P	Q	P	L	E	K	E	N	D	G	19
CCC	GCG	GCC	CCC	CAG	CCG	CTG	GAG	AAG	GAG	AAC	GAC	GGC	77
Y	F	R	K	G	C	N	P	L	A	Q	T	G	32
TAC	TTT	CGG	AAG	GGC	TGT	AAT	CCC	CTT	GCA	CAA	ACC	GGC	116
R	S	K	L	Q	N	Q	R	A	A	L	N	Q	45
CGG	AGT	AAA	TTG	CAG	AAT	CAA	AGA	GCT	GCT	TTG	AAT	CAG	155
Q	I	L	K	A	V	R	M	R	I	G	A	E	58
CAG	ATC	CTG	AAA	GCC	GTG	CGG	ATG	AGG	ATC	GGA	GCG	GAA	194
N	L	L	K	V	A	T	N	S	K	V	R	E	71
AAC	CTT	CTG	AAA	GTG	GCC	ACA	AAC	TCA	AAG	GTG	CGG	GAG	233
Q	V	R	L	E	L	S	F	V	N	S	D	L	84
CAA	GTG	CGG	CTG	GAG	CTG	AGC	TTC	GTC	AAC	TCA	GAC	CTG	272
Q	M	L	K	E	E	L	E	G	L	N	I	S	97
CAG	ATG	CTC	AAG	GAA	GAG	CTG	GAG	GGG	CTG	AAC	ATC	TCG	311
V	G	V	Y	Q	N	T	E	E	A	F	T	I	110
GTG	GGC	GTC	TAT	CAG	AAC	ACA	GAG	GAG	GCA	TTT	ACG	ATT	350
P	L	I	P	L	G	L	K	E	T	K	D	V	124
CCC	CTG	ATT	CCT	CTT	GGC	CTG	AAG	GAA	ACG	AAA	GAC	GTC	389
D	F	A	V	V	L	K	D	F	I	L	E	H	137
GAC	TTT	GCA	GTC	GTC	CTC	AAG	GAT	TTT	ATC	CTG	GAA	CAT	428
Y	S	E	D	G	Y	L	Y	E	D	E	I	A	150
TAC	AGT	GAA	GAT	GGC	TAT	TTA	TAT	GAA	GAT	GAA	ATT	GCA	467
D	L	M	D	L	R	Q	A	C	R	T	P	S	163
GAT	CTT	ATG	GAT	CTG	AGA	CAA	GCT	TGT	CGG	ACG	CCT	AGC	506

FIG. 3A



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R	D	E	A	G	V	E	L	L	M	T	Y	F	176
CGG	GAT	GAG	GCC	GGG	GTG	GAA	CTG	CTG	ATG	ACA	TAC	TTC	545
I	Q	L	G	F	V	E	S	R	F	F	P	P	189
ATC	CAG	CTG	GGC	TTT	GTC	GAG	AGT	CGA	TTC	TTC	CCG	CCC	584
T	R	Q	M	G	L	L	F	T	W	Y	D	S	201
ACA	CGG	CAG	ATG	GGA	CTC	CTG	TTC	ACC	TGG	TAT	GAC	TCT	623
L	T	G	V	P	V	S	Q	Q	N	L	L	L	214
CTC	ACC	GGG	GTT	CCG	GTC	AGC	CAG	CAG	AAC	CTG	CTG	CTG	662
E	K	A	S	V	L	F	N	T	G	A	L	Y	227
GAG	AAG	GCC	AGT	GTC	CTG	TTC	AAC	ACT	GGG	GCC	CTC	TAC	701
T	Q	I	G	T	R	C	D	R	Q	T	Q	A	240
ACC	CAG	ATT	GGG	ACC	CGG	TGC	GAT	CGG	CAG	ACG	CAG	GCT	740
G	L	E	S	A	I	D	A	F	Q	R	A	A	253
GGG	CTG	GAG	AGT	GCC	ATA	GAT	GCC	TTT	CAG	AGA	GCC	GCA	779
G	V	L	N	Y	L	K	D	T	F	T	H	T	266
GGG	GTT	TTA	AAT	TAC	CTG	AAA	GAC	ACA	TTT	ACC	CAT	ACT	818
P	S	Y	D	M	S	P	A	M	L	S	V	L	279
CCA	AGT	TAC	GAC	ATG	AGC	CCT	GCC	ATG	CTC	AGC	GTG	CTC	857
V	K	M	M	L	A	Q	A	Q	E	S	V	F	292
GTC	AAA	ATG	ATG	CTT	GCA	CAA	GCC	CAA	GAA	AGC	GTG	TTT	896
E	K	I	S	L	P	G	I	R	N	E	F	F	305
GAG	AAA	ATC	AGC	CTT	CCT	GGG	ATC	CGG	AAT	GAA	TTC	TTC	935
M	L	V	K	V	A	Q	E	A	A	K	V	G	318
ATG	CTG	GTG	AAG	GTG	GCT	CAG	GAG	GCT	GCT	AAG	GTG	GGA	974
E	V	Y	Q	Q	L	H	A	A	M	S	Q	A	331
GAG	GTC	TAC	CAA	CAG	CTA	CAC	GCA	GCC	ATG	AGC	CAG	GCG	1013
P	V	K	E	N	I	P	Y	S	W	A	S	L	344
CCG	GTG	AAA	GAG	AAC	ATC	CCC	TAC	TCC	TGG	GCC	AGC	TTA	1052
A	C	V	K	A	H	H	Y	A	A	L	A	H	357
GCC	TGC	GTG	AAG	GCC	CAC	CAC	TAC	GCG	GCC	CTG	GCC	CAC	1091
Y	F	T	A	I	L	L	I	D	H	Q	V	K	370
TAC	TTC	ACT	GCC	ATC	CTC	CTC	ATC	GAC	CAC	CAG	GTG	AAG	1130

FIG. 3B



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P	G	T	D	L	D	H	Q	E	K	C	L	S	383
CCA	GGC	ACG	GAT	CTG	GAC	CAC	CAG	GAG	AAG	TGC	CTG	TCC	1169
Q	L	Y	D	H	M	P	E	G	L	T	P	L	396
CAG	CTC	TAC	GAC	CAC	ATG	CCA	GAG	GGG	CTG	ACA	CCC	TTG	1208
A	T	L	K	N	D	Q	Q	R	R	Q	L	G	409
GCC	ACA	CTG	AAG	AAT	GAT	CAG	CAG	CGC	CGA	CAG	CTG	GGG	1247
K	S	H	L	R	R	A	M	A	H	H	E	E	422
AAG	TCC	CAC	TTG	CGC	AGA	GCC	ATG	GCT	CAT	CAC	GAG	GAG	1286
S	V	R	E	A	S	L	C	K	K	L	R	S	435
TCG	GTG	CGG	GAG	GCA	AGC	CTC	TGC	AAG	AAG	CTG	CGG	AGC	1325
I	E	V	L	Q	K	V	L	C	A	A	Q	E	448
ATT	GAG	GTG	CTA	CAG	AAG	GTG	CTG	TGT	GCC	GCA	CAG	GAA	1364
R	S	R	L	T	Y	A	Q	H	Q	E	E	D	461
CGC	TCC	CGG	CTC	ACG	TAC	GCC	CAG	CAC	CAG	GAG	GAG	GAT	1403
D	L	L	N	L	I	D	A	P	S	V	V	A	474
GAC	CTG	CTG	AAC	CTG	ATC	GAC	GCC	CCC	AGT	GTT	GTT	GCT	1442
K	T	E	Q	E	V	D	I	I	L	P	Q	F	487
AAA	ACT	GAG	CAA	GAG	GTT	GAC	ATT	ATA	TTG	CCC	CAG	TTC	1481
S	K	L	T	V	T	D	F	F	Q	K	L	G	500
TCC	AAG	CTG	ACA	GTC	ACG	GAC	TTC	TTC	CAG	AAG	CTG	GGC	1520
P	L	S	V	F	S	A	N	K	R	W	T	P	513
CCC	TTA	TCT	GTG	TTT	TCG	GCT	AAC	AAG	CGG	TGG	ACG	CCT	1559
P	R	S	I	R	F	T	A	E	E	G	D	L	526
CCT	CGA	AGC	ATC	CGC	TTC	ACT	GCA	GAA	GAA	GGG	GAC	TTG	1598
G	F	T	L	R	G	N	A	P	V	Q	V	H	539
GGG	TTC	ACC	TTG	AGA	GGG	AAC	GCC	CCC	GTT	CAG	GTT	CAC	1637
F	L	D	P	Y	C	S	A	S	V	A	G	A	552
TTC	CTG	GAT	CCT	TAC	TGC	TCT	GCC	TCG	GTG	GCA	GGA	GCC	1676
R	E	G	D	Y	I	V	S	I	Q	L	V	D	565
CGG	GAA	GGA	GAT	TAT	ATT	GTC	TCC	ATT	CAG	CTT	GTG	GAT	1715
C	K	W	L	T	L	S	E	V	M	K	L	L	578
TGT	AAG	TGG	CTG	ACG	CTG	AGT	GAG	GTT	ATG	AAG	CTG	CTG	1754

FIG. 3C



Applicants: Shannon et al. AEOMICA-11CON
Application No.: 10/663,470
Filed: September 15, 2003
For : HUMAN GTP-RHO BINDING PROTEIN 2

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K	S	F	G	E	D	E	I	E	M	K	V	V	591
AAG	AGC	TTT	GGC	GAG	GAC	GAG	ATC	GAG	ATG	AAA	GTC	GTG	1793
S	L	L	D	S	T	S	S	M	H	N	K	S	604
AGC	CTC	CTG	GAC	TCC	ACA	TCA	TCC	ATG	CAT	AAT	AAG	AGT	1832
A	T	Y	S	V	G	M	Q	K	T	Y	S	M	617
GCC	ACA	TAC	TCC	GTG	GGA	ATG	CAG	AAA	ACG	TAC	TCC	ATG	1871
I	C	L	A	I	D	D	D	D	K	T	D	K	630
ATC	TGC	TTA	GCC	ATT	GAT	GAT	GAC	GAC	AAA	ACT	GAT	AAA	1910
T	K	K	I	S	K	K	L	S	F	L	S	W	643
ACC	AAG	AAA	ATC	TCC	AAG	AAG	CTT	TCC	TTC	CTG	AGT	TGG	1949
G	T	N	K	N	R	Q	K	S	A	S	T	L	656
GGC	ACC	AAC	AAG	AAC	AGA	CAG	AAG	TCA	GCC	AGC	ACC	TTG	1988
C	L	P	S	V	G	A	A	R	P	Q	V	K	669
TGC	CTC	CCA	TCG	GTC	GGG	GCT	GCA	CGG	CCT	CAG	GTC	AAG	2027
K	K	L	P	S	P	F	S	L	L	N	S	D	682
AAG	AAG	CTG	CCC	TCC	cct	ttc	agc	ctt	ctc	aac	tca	gac	2066
S	S	W	Y	*									686
agt	tct	tgg	tac	taa	tgt	gag	gaa	aca	aac	atg	ttc	agg	2105
ccc	cga	aca	ttt	ccg	gtg	ctg	act	cgg	cct	taa	acg	ttt	2144
gtg	cca	taa	tgg	aaa	ata	tct	atc	tat	ctg	ttg	tca	aat	2183
cct	gtt	ttt	ctc	ata	gtg	taa	act	cac	att	tga	tgt	gtt	2222
ttt	atg	aag	gaa	agt	aac	caa	gaa	acc	tct	agg	aat	tag	2261
tga	aaa	aag	aac	ttt	ttt	gag	gtg	tgt	tac	tat	act	gct	2300
gta	agt	tat	tta	tta	tat	aaa	gta	ttg	taa	ata	gaa	tag	2339
tgt	tga	aga	tat	gaa	ata	tgg	cta	ctt	tta	atg	gtg	aca	2378
att	atg	act	ttt	agt	cac	tat	taa	att	ggg	gtt	acc	tat	2417
atc	agt	aca	att	tgt	agt	tgt	ttc	cag	gtt	tgg	cta	ata	2456
atc	att	cct	taa	cct	aga	att	cag	atg	atc	ctg	gaa	tta	2495
agg	cag	gtc	aga	gga	ctg	taa	tga	tag	aat	taa	att	agt	2534
gtc	act	aaa	aac	tgt	ccc	aaa	gtg	ctg	ctt	cct	aat	agg	2573

FIG. 3D



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aat tca tta acc taa aac aag atg tta cta tta tat cga 2612
tag act atg aat gct att tct aga aaa agt cta gtg cca 2651
aat ttg tct tat taa ata aaa aca atg tag gag cag ctt 2690
ttc ttc tag ttt gat gtc att taa gaa tta cta aca cag 2729
tgg cag tgt tag atg aag atg ctg tct aca agg tag ata 2768
ata tac tgt ttg ata ctc aaa aca ttt ttc att ttg ttt 2807
aaa gta gaa gtt aca taa ttc tat att tta agt ctt ggg 2846
taa aaa agt agt ttt aca ttt tat aaa gta aag atg taa 2885
atg att cag gtt taa agc tct att tga ctt cct ttt ttt 2924
gtt tga gat agc gtc ttg ctg tgt tgc cca ggc tgg agt 2963
gca gtg gtg tga tct cag ctc agt gca acc tcc gcc ccc 3002
tgg gat caa gcg att ctc cta cct cag cct ccc aaa tag 3041
ctg gga cta caa ggt gcc ctc cag cat gcc tgg ctg att 3080
ttt gta ttt tta gtt gag gtg agg ttt cac cat gtt ggc 3119
cag gcg ggt ttc gaa atc ctg acc tca aat gat cca ccc 3158
acc tca gcc tcc caa agt gct ggg att aca ggc atg agc 3197
cac cac aac cgt ccc act att tta ctt ttt aaa atg aca 3236
ttc cta ctg att gat ttt tat ctt gct ata agt tcg atg 3275
aca ccg tga atc taa taa ggt tca ctg ttg aca cag tac 3314
aag tta cat agc taa aat aca tag cat tga aga cta att 3353
tta agg att gac aag agt tta ttt tct att gtg caa tat 3392
ctt aaa gga agc aac cac ctt tgg gaa agt gta tct gct 3431
gct cct agg gcc atg ctt gta tac ata ttt aaa taa aca 3470
tat tca ttt acc cg 3484

FIG. 3E